

## 长链非编码RNA的作用机制及其研究方法

夏天, 肖丙秀, 郭俊明

宁波大学医学院生物化学与分子生物学研究所, 浙江省病理生理学技术研究重点实验室, 宁波 315211

XIA Tian, XIAO Bing-Xiu, GUO Jun-Ming

Department of Biochemistry and Molecular Biology, Ningbo University School of Medicine, Zhejiang Provincial Key Laboratory of Pathophysiology, Ningbo 315211, China

- [摘要](#)
- [参考文献](#)
- [相关文章](#)

Download: [PDF \(611KB\)](#) [HTML \(1KB\)](#) Export: [BibTeX](#) or [EndNote \(RIS\)](#) [Supplementary data](#)

**摘要** 长链非编码RNA(Long non-coding RNA, lncRNA)通过多种机制发挥其生物学功能, 这些机制包括基因印记、染色质重塑、细胞周期调控、剪接调控、mRNA降解和翻译调控等。lncRNA通过这些作用机制在不同水平进行基因表达调控。在研究lncRNA功能的过程中, 研究方法的建立和应用起着非常重要的作用。目前用于lncRNA研究的主要方法有: 微阵列、转录组测序、Northern印迹、实时荧光定量逆转录-聚合酶链反应、荧光原位杂交、RNA干扰和RNA结合蛋白免疫沉淀等。文章着重介绍了3种前沿方法, 即: 在线快速预测RNA与蛋白质相互作用的catRAPID、RNA纯化的染色质分离(Chromatin isolation by RNA purification, ChIRP)以及非编码RNA沉默与定位分析技术(Combined knockdown and localization analysis of non-coding RNAs, c-KLAN)。

**关键词:** [长链非编码RNA](#) [作用机制](#) [基因表达调控](#) [研究方法](#)

**Abstract:** Long non-coding RNAs (lncRNAs) play biological roles through a variety of mechanisms, including genetic imprinting, chromatin remodeling, cell cycle control, splicing regulation, mRNA decay, and translational regulation. lncRNAs are involved in the regulation of gene expression through the above mechanisms in different levels. Establishment and application of research technologies are important in understanding of lncRNAs functions. Microarray, RNA sequencing, Northern blot, real time quantitative reverse transcription-polymerase chain reaction, fluorescence in situ hybridization, RNA interference, and RNA-binding protein immunoprecipitation are major tools of exploring biological functions of lncRNAs. Here, we highlighted three advanced methods, i.e., fast predictions of RNA and protein interactions and domains (catRAPID), chromatin isolation by RNA purification (ChIRP), and combined knockdown and localization analysis of non-coding RNAs (c-KLAN).

**Keywords:** [long non-coding RNAs \(lncRNAs\)](#), [acting mechanisms](#), [gene expression regulation](#), [research methods](#)

收稿日期: 2012-08-08; 出版日期: 2013-03-25

基金资助:

国家自然科学基金项目(编号: 81171660), 宁波市自然科学基金项目(编号: 2012A610207), 宁波市科技创新团队项目(编号: 2011B82014), 宁波市重点学科项目(编号: XKL11D2127)和宁波大学优秀学位论文培育基金项目(编号: PY2012004)资助

通讯作者 郭俊明 Email: junmingguo@yahoo.com

引用本文:

夏天, 肖丙秀, 郭俊明. 长链非编码RNA的作用机制及其研究方法. 遗传, 2013, 35(3): 269-280.

XIA Tian, XIAO Bing-Xiu, GUO Jun-Ming. Acting mechanisms and research methods of long noncoding RNAs. HEREDITAS, 2013, V35(3): 269-280.

链接本文:

[http://www.chinagene.cn/Jwk\\_yc/CN/10.3724/SP.J.1005.2013.00269](http://www.chinagene.cn/Jwk_yc/CN/10.3724/SP.J.1005.2013.00269) 或 [http://www.chinagene.cn/Jwk\\_yc/CN/Y2013/V35/I3/269](http://www.chinagene.cn/Jwk_yc/CN/Y2013/V35/I3/269)

[1] Spizzo R, Almeida MI, Colombatti A, Calin GA. Long non-coding RNAs and cancer: a new frontier of translational research? *Oncogene*, 2012, 31(43): 4577-4587.

[2] Wapinski O, Chang HY. Long noncoding RNAs and human disease. *Trends Cell Biol*, 2011, 21(6): 354-361. 

[3] 于红. 表观遗传学: 生物细胞非编码RNA调控的研究进展. 遗传, 2009, 31(11): 1077-1086. [浏览](#)

[4] 张绍峰, 李晓荣, 孙传宝, 何玉科. 植物非编码RNA调控春化作用的表观遗传. 遗传, 2012, 34(7): 829-834. [浏览](#)

[5] 孙强, 黄红艳, 韩骅. ncRNA候选基因spt1的克隆与初步分析. 遗传学报, 2004, 31(5): 485-488. [浏览](#)











[6] Xiao B, Zhang XJ, Li Y, Tang ZL, Yang SL, Mu YL, Cui WT, Ao H, Li K. Identification, bioinformatic analysis and expression profiling of


### Service

















- ▶ [把本文推荐给朋友](#)
- ▶ [加入我的书架](#)
- ▶ [加入引用管理器](#)
- ▶ [Email Alert](#)
- ▶ [RSS](#)

### 作者相关文章

- ▶ [夏天](#)
- ▶ [肖丙秀](#)
- ▶ [郭俊明](#)

- [7] Wutz A, Rasmussen TP, Jaenisch R. Chromosomal silencing and localization are mediated by different domains of Xist RNA. *Nat Genet*, 2002, 30(2): 167-174. 
- [8] Gong C, Maquat LE. lncRNAs transactivate STAU1-mediated mRNA decay by duplexing with 3' UTRs via Alu elements. *Nature*, 2011, 470(7333): 284-288.
- [9] Clemson CM, Hutchinson JN, Sara SA, Ensminger AW, Fox AH, Chess A, Lawrence JB. An architectural role for a nuclear noncoding RNA: NEAT1 RNA is essential for the structure of paraspeckles. *Mol Cell*, 2009, 33(6): 717-726. 
- [10] Gupta RA, Shah N, Wang KC, Kim J, Horlings HM, Wong DJ, Tsai MC, Hung T, Argani P, Rinn JL, Wang YL, Brzoska P, Kong B, Li R, West RB, van de Vijver MJ, Sukumar S, Chang HY. Long non-coding RNA HOTAIR reprograms chromatin state to promote cancer metastasis. *Nature*, 2010, 464(7291): 1071-1076.
- [11] Tsai MC, Manor O, Wan Y, Mosammamaparast N, Wang JK, Lan F, Shi Y, Segal E, Chang HY. Long noncoding RNA as modular scaffold of histone modification complexes. *Science*, 2010, 329(5992): 689-693.
- [12] 宋皓军, 俞秀冲, 夏天, 郭俊明, 肖丙秀. 长链非编码RNA与肿瘤的关系及其临床价值. *中国细胞生物学学报*, 2012, 34(7): 704-712.
- [13] Mercer TR, Dinger ME, Mattick JS. Long non-coding RNAs: insights into functions. *Nat Rev Genet*, 2009, 10(3): 155-159. 
- [14] Wang KC, Chang HY. Molecular mechanisms of long noncoding RNAs. *Mol Cell*, 2011, 43(6): 904-914. 
- [15] Erdmann VA, Szymanski M, Hochberg A, de Groot N, Barciszewski J. Non-coding, mRNA-like RNAs database Y2K. *Nucleic Acids Res*, 2000, 28(1): 197-200. 
- [16] Mituyama T, Yamada K, Hattori E, Okida H, Ono Y, Terai G, Yoshizawa A, Komori T, Asai K. The Functional RNA Database 3. 0: databases to support mining and annotation of functional RNAs. *Nucleic Acids Res*, 2009, 37(Suppl. 1): D89-D92.
- Dinger ME, Pang KC, Mercer TR, Crowe ML, Grimmond SM, Mattick JS. NRED: a database of long noncoding RNA expression. *Nucleic Acids Res*, 2009, 37(Suppl. 1): D122-D126.
- [17] Amaral PP, Clark MB, Gascoigne DK, Dinger ME, Mattick JS. lncRNadb: a reference database for long noncoding RNAs. *Nucleic Acids Res*, 2011, 39(Suppl. 1): D146-D151.
- [18] Liao Q, Xiao H, Bu DC, Xie CY, Miao RY, Luo HT, Zhao GG, Yu KT, Zhao HT, Skogerbø G, Chen RS, Wu ZD, Liu CN, Zhao Y. ncFANs: a web server for functional annotation of long non-coding RNAs. *Nucleic Acids Res*, 2011, 39(Suppl. 2): W118-W124.
- [19] Bu DC, Yu KT, Sun SL, Xie CY, Skogerbø G, Miao RY, Xiao H, Liao Q, Luo HT, Zhao GG, Zhao HT, Liu ZY, Liu CN, Chen RS, Zhao Y. NONCODE v3. 0: integrative annotation of long noncoding RNAs. *Nucleic Acids Res*, 2012, 40(D1): D210-D215.
- [20] Muers M. RNA: Genome-wide views of long non-coding RNAs. *Nat Rev Genet*, 2011, 12(11): 742.
- [21] Khalil AM, Guttman M, Huarte M, Garber M, Raj A, Rivea Morales D, Thomas K, Presser A, Bernstein BE, van Oudenaarden A, Regev A, Lander ES, Rinn JL. Many human large intergenic noncoding RNAs associate with chromatin-modifying complexes and affect gene expression. *Proc Natl Acad Sci USA*, 2009, 106(28): 11667-11672. 
- [22] Chu C, Qu K, Zhong FL, Artandi SE, Chang HY. Genomic maps of long noncoding RNA occupancy reveal principles of RNA-chromatin interactions. *Mol Cell*, 2011, 44(4): 667-678. 
- [23] Cabili MN, Trapnell C, Goff L, Koziol M, Tazon-Vega B, Regev A, Rinn JL. Integrative annotation of human large intergenic noncoding RNAs reveals global properties and specific subclasses. *Genes Dev*, 2011, 25(18): 1915-1927. 
- [24] Arney KL. H19 and Igf2--enhancing the confusion? *Trends Genet*, 2003, 19(1): 17-23.
- [25] Lee JT. The X as model for RNA' s niche in epigenomic regulation. *Cold Spring Harb Perspect Biol*, 2010, 2(9): a003749.
- [26] Stavropoulos N, Lu N, Lee JT. A functional role for Tsix transcription in blocking Xist RNA accumulation but not in X-chromosome choice. *Proc Natl Acad Sci USA*, 2001, 98(18): 10232-10237. 
- [27] Yap KL, Li SD, Muñoz-Cabello AM, Raguz S, Zeng L, Mujtaba S, Gil J, Walsh MJ, Zhou MM. Molecular interplay of the noncoding RNA ANRIL and methylated histone H3 lysine 27 by polycomb CBX7 in transcriptional silencing of *INK4a*. *Mol Cell*, 2010, 38(5): 662-674. 
- [28] Kino T, Hurt DE, Ichijo T, Nader N, Chrousos GP. Noncoding RNA gas5 is a growth arrest-and starvation- associated repressor of the glucocorticoid receptor. *Sci Signal*, 2010, 3(107): ra8.
- [29] Huarte M, Guttman M, Feldser D, Garber M, Koziol MJ, Kenzelmann-Broz D, Khalil AM, Zuk O, Amit I, Rabani M, Attardi LD, Regev A, Lander ES, Jacks T, Rinn JL. A large intergenic noncoding RNA induced by p53 mediates global gene repression in the p53 response. *Cell*, 2010, 142(3): 409-419.
- [30] Hung T, Wang YL, Lin MF, Koegel AK, Kotake Y, Grant GD, Horlings HM, Shah N, Umbricht C, Wang P, Kong B, Langerød A, Børresen-Dale AL, Kim SK, van de Vijver M, Sukumar S, Whitfield ML, Kellis M, Xiong Y, Wong DJ, Chang HY. Extensive and coordinated transcription of noncoding RNAs within cell-cycle promoters. *Nat Genet*, 2011, 43(7): 621-629. 
- [31] Jolly C, Lakhota SC. Human sat III and *Drosophila* hsrw transcripts: a common paradigm for regulation of nuclear RNA processing in stressed cells. *Nucleic Acids Res*, 2006, 34(19): 5508-5514. 
- [32] Tripathi V, Ellis JD, Shen Z, Song DY, Pan Q, Watt AT, Freier SM, Bennett CF, Sharma A, Bubulya PA, Blencowe BJ, Prasanth SG, Prasanth

KV. The nuclear-retained noncoding RNA MALAT1 regulates alternative splicing by modulating SR splicing factor phosphorylation. *Mol Cell*, 2010, 39(6): 925-938. 

- [33] Faghihi MA, Modarresi F, Khalil AM, Wood DE, Sahagan BG, Morgan TE, Finch CE, St Laurent G III, Kenny PJ, Wahlestedt C. Expression of a noncoding RNA is elevated in Alzheimer's disease and drives rapid feed-forward regulation of  $\beta$ -secretase. *Nat Med*, 2008, 14(7): 723-730. 
- [34] 赵丽霞, 赵高平, 周欢敏. 哺乳动物印记域DLK1-DIO3的研究进展. *遗传*, 2010, 32(8): 769-778. [浏览](#)
- [35] Gibb EA, Brown CJ, Lam WL. The functional role of long non-coding RNA in human carcinomas. *Mol Cancer*, 2011, 10: 38. 
- [36] Kelley RL, Kuroda MI. Noncoding RNA genes in dosage compensation and imprinting. *Cell*, 2000, 103(1): 9-12.
- [37] Gabory A, Jammes H, Dandolo L. The H19 locus: role of an imprinted non-coding RNA in growth and development. *Bioessays*, 2010, 32(6): 473-480.
- [38] Smits G, Mungall AJ, Griffiths-Jones S, Smith P, Beury D, Matthews L, Rogers J, Pask AJ, Shaw G, Vandeberg JL, Mccarrey JR, Renfree MB, Reik W, Dunham I. Conservation of the H19 noncoding RNA and H19-IGF2 imprinting mechanism in therians. *Nat Genet*, 2008, 40(8): 971-976. 
- [39] Zhang YH, Tycko B. Monoallelic expression of the human H19 gene. *Nat Genet*, 1992, 1(1): 40-44. 
- [40] Hark AT, Schoenherr CJ, Katz DJ, Ingram RS, Levorse JM, Tilghman SM. CTCF mediates methylation-sensitive enhancer-blocking activity at the *H19/Igf2* locus. *Nature*, 2000, 405(6785): 486-489.
- [41] Schoenherr CJ, Levorse JM, Tilghman SM. CTCF maintains differential methylation at the *Igf2/H19* locus. *Nat Genet*, 2003, 33(1): 66-69. 
- [42] Zhao J, Sun BK, Erwin JA, Song JJ, Lee JT. Polycomb proteins targeted by a short repeat RNA to the mouse X chromosome. *Science*, 2008, 322(5902): 750-756.
- [43] Lee JT, Davidow LS, Warshawsky D. Tsix, a gene antisense to Xist at the X-inactivation centre. *Nat Genet*, 1999, 21(4): 400-404. 
- [44] Faust T, Frankel A, D'orso I. Transcription control by long non-coding RNAs. *Transcription*, 2012, 3(2): 78-86. 
- [45] Rinn JL, Kertesz M, Wang JK, Squazzo SL, Xu X, Brugmann SA, Goodnough LH, Helms JA, Farnham PJ, Segal E, Chang HY. Functional demarcation of active and silent chromatin domains in human HOX loci by noncoding RNAs. *Cell*, 2007, 129(7): 1311-1323.
- [46] Kotake Y, Nakagawa T, Kitagawa K, Suzuki S, Liu N, Kitagawa M, Xiong Y. Long non-coding RNA ANRIL is required for the PRC2 recruitment to and silencing of p15INK4B tumor suppressor gene. *Oncogene*, 2011, 30(16): 1956-1962. 
- [47] Mourtada-Maarabouni M, Pickard MR, Hedge VL, Farzaneh F, Williams GT. GAS5, a non-protein-coding RNA, controls apoptosis and is downregulated in breast cancer. *Oncogene*, 2009, 28(2): 195-208. 
- [48] Wilusz JE, Freier SM, Spector DL. 3' end processing of a long nuclear-retained noncoding RNA yields a tRNA-like cytoplasmic RNA. *Cell*, 2008, 135(5): 919-932.
- [49] Bernard D, Prasanth KV, Tripathi V, Colasse S, Nakamura T, Xuan ZY, Zhang MQ, Sedel F, Jourden L, Couplier F, Triller A, Spector DL, Bessis A. A long nuclear-retained non-coding RNA regulates synaptogenesis by modulating gene expression. *EMBO J*, 2010, 29(18): 3082-3093. 
- [50] Tollervey JR, Curk T, Rogelj B, Briese M, Cereda M, Kaykici M, König J, Hortobágyi T, Nishimura AL, ?upunski V, Patani R, Chandran S, Rot G, Zupan B, Shaw CE, Ule J. Characterizing the RNA targets and position- dependent splicing regulation by TDP-43. *Nat Neurosci*, 2011, 14(4): 452-458. 
- [51] Maquat LE. Nonsense-mediated mRNA decay: splicing, translation and mRNP dynamics. *Nat Rev Mol Cell Biol*, 2004, 5(2): 89-99.
- [52] Kim YK, Furic L, Desgroseillers L, Maquat LE. Mammalian Staufen1 recruits Upf1 to specific mRNA 3'UTRs so as to elicit mRNA decay. *Cell*, 2005, 120(2): 195-208.
- [53] Kim YK, Furic L, Parisien M, Major F, DesGroseillers L, Maquat LE. Staufen1 regulates diverse classes of mammalian transcripts. *EMBO J*, 2007, 26(11): 2670-2681. 
- [54] Hardy J, Selkoe DJ. The amyloid hypothesis of Alzheimer's disease: progress and problems on the road to therapeutics. *Science*, 2002, 297(5580): 353-356.
- [55] Yoon JH, Abdelmohsen K, Srikantan S, Yang XL, Martindale JL, De S, Huarte M, Zhan M, Becker KG, Gorospe M. LincRNA-p21 suppresses target mRNA translation. *Mol Cell*, 2012, 47(4): 648-655. 
- [56] Yan B, Wang ZH, Guo JT. The research strategies for probing the function of long noncoding RNAs. *Genomics*, 2012, 99(2): 76-80. 
- [57] Dinger ME, Amaral PP, Mercer TR, Pang KC, Bruce SJ, Gardiner BB, Askarian-Amiri ME, Ru KL, Soldà G, Simons C, Sunkin SM, Crowe ML, Grimmond SM, Perkins AC, Mattick JS. Long noncoding RNAs in mouse embryonic stem cell pluripotency and differentiation. *Genome Res*, 2008, 18(9): 1433-1445. 
- [58] Mortazavi A, Williams BA, Mccue K, Schaeffer L, Wold B. Mapping and quantifying mammalian transcriptomes by RNA-Seq. *Nat Methods*, 2008, 5(7): 621-628. 
- [59] Oslash:rom UA, Derrien T, Beringer M, Gumireddy K, Gardini A, Bussotti G, Lai F, Zytnicki M, Notredame C, Huang QH, Guigo R, Shiekhattar R.

- [60] Lin MY, Pedrosa E, Shah A, Hrabovsky A, Maqbool S, Zheng DY, Lachman HM. RNA-Seq of human neurons derived from iPS cells reveals candidate long non-coding RNAs involved in neurogenesis and neuropsychiatric disorders. *PLoS One*, 2011, 6(9): e23356.
- [61] Alwine JC, Kemp DJ, Stark GR. Method for detection of specific RNAs in agarose gels by transfer to diazobenzyloxymethyl-paper and hybridization with DNA probes. *Proc Natl Acad Sci USA*, 1977, 74(12): 5350-5354. 
- [62] Heid CA, Stevens J, Livak KJ, Williams PM. Real time quantitative PCR. *Genome Res*, 1996, 6(10): 986-994. 
- [63] Furuno M, Pang KC, Ninomiya N, Fukuda S, Frith MC, Bult C, Kai C, Kawai J, Carninci P, Hayashizaki Y, Mattick JS, Suzuki H. Clusters of internally primed transcripts reveal novel long noncoding RNAs. *PLoS Genet*, 2006, 2(4): e37.
- [64] Rudkin GT, Stollar BD. High resolution detection of DNA-RNA hybrids in situ by indirect immunofluorescence. *Nature*, 1977, 265(5593): 472-473.
- [65] Fire A, Xu SQ, Montgomery MK, Kostas SA, Driver SE, Mello CC. Potent and specific genetic interference by double-stranded RNA in *Caenorhabditis elegans*. *Nature*, 1998, 391(6669): 806-811.
- [66] Pandey RR, Mondal T, Mohammad F, Enroth S, Redrup L, Komorowski J, Nagano T, Mancini-Dinardo D, Kanduri C. *Kcnq1ot1* antisense noncoding RNA mediates lineage-specific transcriptional silencing through chromatin-level regulation. *Mol Cell*, 2008, 32(2): 232-246. 
- [67] Keene JD, Komisarow JM, Friedersdorf MB. RIP-Chip: the isolation and identification of mRNAs, microRNAs and protein components of ribonucleoprotein complexes from cell extracts. *Nat Protoc*, 2006, 1(1): 302-307. 
- [68] Zhao J, Ohsumi TK, Kung JT, Ogawa Y, Grau DJ, Sarma K, Song JJ, Kingston RE, Borowsky M, Lee JT. Genome-wide identification of polycomb-associated RNAs by RIP-seq. *Mol Cell*, 2010, 40(6): 939-953. 
- [69] Bellucci M, Agostini F, Masin M, Tartaglia GG. Predicting protein associations with long noncoding RNAs. *Nat Methods*, 2011, 8(6): 444-445. 
- [70] Chakraborty D, Kappei D, Theis M, Nitzsche A, Ding L, Paszkowski-Rogacz M, Surendranath V, Berger N, Schulz H, Saar K, Hubner N, Buchholz F. Combined RNAi and localization for functionally dissecting long noncoding RNAs. *Nat Methods*, 2012, 9(4): 360-362. 
- [71] Wu T, Wang J, Liu C, Zhang Y, Shi B, Zhu X, Zhang Z, Skogerbo G, Chen L, Lu H, Zhao Y, Chen R. NPInter: the noncoding RNAs and protein related biomacromolecules interaction database. *Nucleic Acids Res*, 2006, 34(Suppl 1): D150-D152.
- [72] Maenner S, Blaud M, Fouillen L, Savoye A, Marchand V, Dubois A, Sanglier-Cianferani S, van Dorsselaer A, Clerc P, Avner P, Visvikis A, Branlant C. 2-D structure of the A region of Xist RNA and its implication for PRC2 association. *PLoS Biol*, 2010, 8(1): e1000276.
- [73] Chu C, Quinn J, Chang HY. Chromatin isolation by RNA purification (ChIRP). *J Vis Exp*, 2012, (61): e3912.
- [74] Franke A, Baker BS. The rox1 and rox2 RNAs are essential components of the compensasome, which mediates dosage compensation in *Drosophila*. *Mol Cell*, 1999, 4(1): 117-122. 
- [75] Yang D, Buchholz F, Huang ZD, Goga A, Chen CY, Brodsky FM, Bishop JM. Short RNA duplexes produced by hydrolysis with *Escherichia coli* RNase III mediate effective RNA interference in mammalian cells. *Proc Natl Acad Sci USA*, 2002, 99(15): 9942-9947. 
- [76] Kittler R, Surendranath V, Heninger AK, Slabicki M, Theis M, Putz G, Franke K, Caldarelli A, Grabner H, Kozak K, Wagner J, Rees E, Korn B, Frenzel C, Sachse C, Sonnichsen B, Guo J, Schelter J, Burchard J, Linsley PS, Jackson A L, Habermann B, Buchholz F. Genome-wide resources of endoribonuclease-prepared short interfering RNAs for specific loss-of-function studies. *Nat Methods*, 2007, 4(4): 337-344.
- [77] Henschel A, Buchholz F, Habermann B. DEQOR: a web-based tool for the design and quality control of siRNAs. *Nucleic Acids Res*, 2004, 32(Suppl 2): W113-W120.
- [78] Itzkovitz S, van Oudenaarden A. Validating transcripts with probes and imaging technology. *Nat Methods*, 2011, 8(4 Suppl.): S12-S19.
- [79] Baker M. Long noncoding RNAs: the search for function. *Nat Methods*, 2011, 8(5): 379-383. 
- [80] Bánfalvi B, Jia H, Khatun J, Wood E, Risk B, Gundling WE Jr, Kundaje A, Gunawardena HP, Yu YB, Xie L, Krajewski K, Strahl BD, Chen X, Bickel P, Giddings MC, Brown JB, Lipovich L. Long noncoding RNAs are rarely translated in two human cell lines. *Genome Res*, 2012, 22(9): 1646-1657. 
- [81] Paige JS, Wu KY, Jaffrey SR. RNA mimics of green fluorescent protein. *Science*, 2011, 333(6042): 642-646.
- [82] Mercer TR, Gerhardt DJ, Dinger ME, Crawford J, Trapnell C, Jeddloh JA, Mattick JS, Rinn JL. Targeted RNA sequencing reveals the deep complexity of the human transcriptome. *Nat Biotechnol*, 2012, 30(1): 99-104.

- [1] 张韬 杨足君.植物基因组DNase I超敏感位点的研究进展[J]. 遗传, 2013,35(7): 867-874
- [2] 李泽琴, 李静晓, 张根发.植物抗坏血酸过氧化物酶的表达调控以及对非生物胁迫的耐受作用[J]. 遗传, 2013,35(1): 45-54
- [3] 罗茂, 张志明, 高健, 曾兴, 潘光堂.miR319在植物器官发育中的调控作用[J]. 遗传, 2011,33(11): 1203-1211
- [4] 孟雅楠, 孟丽军, 宋亚娟, 刘美玲, 张秀军.小RNA分子与精子发生调控[J]. 遗传, 2011,33(1): 9-16
- [5] 程龙, 黄翠芬, 叶棋浓.乳腺癌中雌激素受体 $\alpha$ 表达水平调节的分子机制[J]. 遗传, 2010,32(3): 191-197
- [6] 丁艳菲, 王光钺, 傅亚萍, 朱诚.miR398在植物逆境胁迫应答中的作用[J]. 遗传, 2010,32(2): 129-134
- [7] 杨文杰, 吴燕民, 唐益雄.大豆转录因子基因*GmMYB6*的表达及功能分析[J]. 遗传, 2009,31(6): 645-653

- [8] 谭建新, 孙玉洁. 表观基因组学研究方法与评价[J]. 遗传, 2009,31(1): 3-12
- [9] 杨冬, 姜颖, 贺福初. KAP-1: 转录调控中的一个桥梁分子[J]. 遗传, 2007,29(2): 131-131-136
- [10] 贺道华, 张献龙. 数量性状由表型变异到基因发现的研究进展[J]. 遗传, 2006,28(12): 1613-1613-1618
- [11] 李艳凤, 张强, 朱大海. 泛素介导的蛋白质降解与肿瘤发生[J]. 遗传, 2006,28(12): 1591-1591-1596
- [12] 孙业盈, 吕彦, 董春林, 王平荣, 黄晓群, 邓晓建. 水稻Wx基因表达调控的研究进展[J]. 遗传, 2005,27(6): 1013-1019
- [13] 王水良, 傅继梁. 核受体的研究进展[J]. 遗传, 2004,31(4): 420-429
- [14] 周迅雷, 胡新立, 吴鹤龄. Nodal基因顺式调控序列的分析[J]. 遗传, 1999,26(2): 142-149
- [15] 赵友阳, 敖世洲. 酵母PHO80基因的克隆、表达及功能分析[J]. 遗传, 1996,23(2): 142-148